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SEQUENCE LISTING

<110> CHUGAI SEIYAKU KABUSHIKI KAISHA

<120> METHODS FOR PRODUCING ANTIBODIES

<130> C1-A0210Y1P

<140>

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<150> JP 2002-164834

<151> 2002-06-05

<150> JP 2002-180351

<151> 2002-06-20

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<170> PatentIn Ver. 2.1

<210> 1

<211> 28

<212> DNA

<213> Artificial Sequence

2 / 1 0

<220>

<223> Description of Artificial Sequence:an artificially
synthesized primer sequence

<400> 1

gaattccacc atggttaagcg ctattgtt

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<210> 2

<211> 26

<212> DNA

<213> Artificial Sequence

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<223> Description of Artificial Sequence:an artificially
synthesized primer sequence

<400> 2

gaattcttaa tattgtctat tacggt

26

<210> 3

<211> 1539

<212> DNA

<213> Baculovirus

3 / 1 0

<220>

<221> CDS

<222> (1).. (1539)

<400> 3

atg gta agc gct att gtt tta tat gtg ctt ttg gcg gcg gcg gcg cat 48

Met Val Ser Ala Ile Val Leu Tyr Val Leu Leu Ala Ala Ala Ala His

1 5 10 15

tct gcc ttt gcg gcg gag cac tgc aac gcg caa atg aag acg ggt ccg 96

Ser Ala Phe Ala Ala Glu His Cys Asn Ala Gln Met Lys Thr Gly Pro

20 25 30

tac aag att aaa aac ttg gac att acc ccg ccc aag gaa acg ctg caa 144

Tyr Lys Ile Lys Asn Leu Asp Ile Thr Pro Pro Lys Glu Thr Leu Gln

35 40 45

aag gac gtg gaa atc acc atc gtg gag acg gac tac aac gaa aac gtg 192

Lys Asp Val Glu Ile Thr Ile Val Glu Thr Asp Tyr Asn Glu Asn Val

50 55 60

att atc ggc tac aag ggg tac tac cag gcg tat gcg tac aac ggc ggc 240

Ile Ile Gly Tyr Lys Gly Tyr Tyr Gln Ala Tyr Ala Tyr Asn Gly Gly

65 70 75 80

tcg ctg gat ccc aac aca cgc gtc gaa gaa acc atg aaa acg ctg aat 288

4 / 1 0

Ser Leu Asp Pro Asn Thr Arg Val Glu Glu Thr Met Lys Thr Leu Asn

85

90

95

gtg ggc aaa gag gat ttg ctt atg tgg agc atc agg cag cag tgc gag 336

Val Gly Lys Glu Asp Leu Leu Met Trp Ser Ile Arg Gln Gln Cys Glu

100

105

110

gtg ggc gaa gag ctg atc gac cgt tgg ggc agt gac agc gac gac tgt 384

Val Gly Glu Glu Leu Ile Asp Arg Trp Gly Ser Asp Ser Asp Asp Cys

115

120

125

ttt cgc gac aac gag ggc cgc ggc cag tgg gtc aaa ggc aaa gag ttg 432

Phe Arg Asp Asn Glu Gly Arg Gly Gln Trp Val Lys Gly Lys Glu Leu

130

135

140

gtg aag cgg cag aat aac aat cac ttt gcg cac cac acg tgc aac aaa 480

Val Lys Arg Gln Asn Asn Asn His Phe Ala His His Thr Cys Asn Lys

145

150

155

160

tcg tgg cga tgc ggc att tcc act tcg aaa atg tac agc agg ctc gag 528

Ser Trp Arg Cys Gly Ile Ser Thr Ser Lys Met Tyr Ser Arg Leu Glu

165

170

175

tgc cag gac gac acg gac gag tgc cag gta tac att ttg gac gct gag 576

Cys Gln Asp Asp Thr Asp Glu Cys-Gln Val Tyr Ile Leu Asp Ala Glu

180

185

190

ggc aac ccc atc aac gtg acc gtg gac act gtg ctt cat cga gac ggc 624
 Gly Asn Pro Ile Asn Val Thr Val Asp Thr Val Leu His Arg Asp Gly
 195 200 205

gtg agt atg att ctc aaa caa aag tct acg ttc acc acg cgc caa ata 672
 Val Ser Met Ile Leu Lys Gln Lys Ser Thr Phe Thr Thr Arg Gln Ile
 210 215 220

aaa gct gcg tgt ctg ctc att aaa gat gac aaa aat aac ccc gag tcg 720
 Lys Ala Ala Cys Leu Leu Ile Lys Asp Asp Lys Asn Asn Pro Glu Ser
 225 230 235 240

gtg aca cgc gaa cac tgt ttg att gac aat gat ata tat gat ctt tct 768
 Val Thr Arg Glu His Cys Leu Ile Asp Asn Asp Ile Tyr Asp Leu Ser
 245 250 255

aaa aac acg tgg aac tgc aag ttt aac aga tgc att aaa cgc aaa gtc 816
 Lys Asn Thr Trp Asn Cys Lys Phe Asn Arg Cys Ile Lys Arg Lys Val
 260 265 270

gag cac cga gtc aag aag cgg ccg ccc act tgg cgc cac aac gtt aga 864
 Glu His Arg Val Lys Lys Arg Pro Pro Thr Trp Arg His Asn Val Arg
 275 280 285

gcc aag tac aca gag gga gac act gcc acc aaa ggc gac ctg atg cat 912

Ala Lys Tyr Thr Glu Gly Asp Thr Ala Thr Lys Gly Asp Leu Met His

290

295

300

att caa gag gag ctg atg tac gaa aac gat ttg ctg aaa atg aac att 960

Ile Gln Glu Glu Leu Met Tyr Glu Asn Asp Leu Leu Lys Met Asn Ile

305

310

315

320

gag ctg atg cat gcg cac atc aac aag cta aac aat atg ctg cac gac 1008

Glu Leu Met His Ala His Ile Asn Lys Leu Asn Asn Met Leu His Asp

325

330

335

ctg ata gtc tcc gtg gcc aag gtg gac gag cgt ttg att ggc aat ctc 1056

Leu Ile Val Ser Val Ala Lys Val Asp Glu Arg Leu Ile Gly Asn Leu

340

345

350

atg aac aac tct gtt tct tca aca ttt ttg tgc gac gac acg ttt ttg 1104

Met Asn Asn Ser Val Ser Ser Thr Phe Leu Ser Asp Asp Thr Phe Leu

355

360

365

ctg atg ccg tgc acc aat ccg ccg gca cac acc agt aat tgc tac aac 1152

Leu Met Pro Cys Thr Asn Pro Pro Ala His Thr Ser Asn Cys Tyr Asn

370

375

380

aac agc atc tac aaa gaa ggg cgt tgg gtg gcc aac acg gac tgc tgc 1200

Asn Ser Ile Tyr Lys Glu Gly Arg Trp Val Ala Asn Thr Asp Ser Ser

385

390

395

400

caa tgc ata gat ttt agc aac tac aag gaa cta gca att gac gac gac 1248

Gln Cys Ile Asp Phe Ser Asn Tyr Lys Glu Leu Ala Ile Asp Asp Asp

405

410

415

gtc gag ttt tgg atc ccg acc atc ggc aac acg acc tat cac gac agt 1296

Val Glu Phe Trp Ile Pro Thr Ile Gly Asn Thr Thr Tyr His Asp Ser

420

425

430

tgg aaa gat gcc agc ggc tgg tcg ttt att gcc caa caa aaa agc aac 1344

Trp Lys Asp Ala Ser Gly Trp Ser Phe Ile Ala Gln Gln Lys Ser Asn

435

440

445

ctc ata acc acc atg gag aac acc aag ttt ggc ggc gtc ggc acc agt 1392

Leu Ile Thr Thr Met Glu Asn Thr Lys Phe Gly Gly Val Gly Thr Ser

450

455

460

ctg agc gac atc act tcc atg gct gaa ggc gaa ttg gcc gct aaa ttg 1440

Leu Ser Asp Ile Thr Ser Met Ala Glu Gly Glu Leu Ala Ala Lys Leu

465

470

475

480

act tcg ttc atg ttt ggt cat gta gtt aac ttt gta att ata tta att 1488

Thr Ser Phe Met Phe Gly His Val Val Asn Phe Val Ile Ile Leu Ile

485

490

495

gtg att tta ttt ttg tac tgt atg att aga aac cgt aat aga caa tat 1536

8 / 1 0

Val Ile Leu Phe Leu Tyr Cys Met Ile Arg Asn Arg Asn Arg Gln Tyr

500

505

510

taa

1539

<210> 4

<211> 512

<212> PRT

<213> Baculovirus

<400> 4

Met Val Ser Ala Ile Val Leu Tyr Val Leu Leu Ala Ala Ala Ala His

1

5

10

15

Ser Ala Phe Ala Ala Glu His Cys Asn Ala Gln Met Lys Thr Gly Pro

20

25

30

Tyr Lys Ile Lys Asn Leu Asp Ile Thr Pro Pro Lys Glu Thr Leu Gln

35

40

45

Lys Asp Val Glu Ile Thr Ile Val Glu Thr Asp Tyr Asn Glu Asn Val

50

55

60

Ile Ile Gly Tyr Lys Gly Tyr Tyr Gln Ala Tyr Ala Tyr Asn Gly Gly

65

70

75

80

Ser Leu Asp Pro Asn Thr Arg Val Glu Glu Thr Met Lys Thr Leu Asn

85

90

95

Val Gly Lys Glu Asp Leu Leu Met Trp Ser Ile Arg Gln Gln Cys Glu

100	105	110
Val Gly Glu Glu Leu Ile Asp Arg Trp Gly Ser Asp Ser Asp Asp Cys		
115	120	125
Phe Arg Asp Asn Glu Gly Arg Gly Gln Trp Val Lys Gly Lys Glu Leu		
130	135	140
Val Lys Arg Gln Asn Asn Asn His Phe Ala His His Thr Cys Asn Lys		
145	150	155
Ser Trp Arg Cys Gly Ile Ser Thr Ser Lys Met Tyr Ser Arg Leu Glu		
165	170	175
Cys Gln Asp Asp Thr Asp Glu Cys Gln Val Tyr Ile Leu Asp Ala Glu		
180	185	190
Gly Asn Pro Ile Asn Val Thr Val Asp Thr Val Leu His Arg Asp Gly		
195	200	205
Val Ser Met Ile Leu Lys Gln Lys Ser Thr Phe Thr Thr Arg Gln Ile		
210	215	220
Lys Ala Ala Cys Leu Leu Ile Lys Asp Asp Lys Asn Asn Pro Glu Ser		
225	230	235
Val Thr Arg Glu His Cys Leu Ile Asp Asn Asp Ile Tyr Asp Leu Ser		
245	250	255
Lys Asn Thr Trp Asn Cys Lys Phe Asn Arg Cys Ile Lys Arg Lys Val		
260	265	270
Glu His Arg Val Lys Lys Arg Pro Pro Thr Trp Arg His Asn Val Arg		
275	280	285
Ala Lys Tyr Thr Glu Gly Asp Thr Ala Thr Lys Gly Asp Leu Met His		
290	295	300
Ile Gln Glu Glu Leu Met Tyr Glu Asn Asp Leu Leu Lys Met Asn Ile		

1 0 / 1 0

305	310	315	320
Glu Leu Met His Ala His Ile Asn Lys Leu Asn Asn Met Leu His Asp			
325	330	335	
Leu Ile Val Ser Val Ala Lys Val Asp Glu Arg Leu Ile Gly Asn Leu			
340	345	350	
Met Asn Asn Ser Val Ser Ser Thr Phe Leu Ser Asp Asp Thr Phe Leu			
355	360	365	
Leu Met Pro Cys Thr Asn Pro Pro Ala His Thr Ser Asn Cys Tyr Asn			
370	375	380	
Asn Ser Ile Tyr Lys Glu Gly Arg Trp Val Ala Asn Thr Asp Ser Ser			
385	390	395	400
Gln Cys Ile Asp Phe Ser Asn Tyr Lys Glu Leu Ala Ile Asp Asp Asp			
405	410	415	
Val Glu Phe Trp Ile Pro Thr Ile Gly Asn Thr Thr Tyr His Asp Ser			
420	425	430	
Trp Lys Asp Ala Ser Gly Trp Ser Phe Ile Ala Gln Gln Lys Ser Asn			
435	440	445	
Leu Ile Thr Thr Met Glu Asn Thr Lys Phe Gly Gly Val Gly Thr Ser			
450	455	460	
Leu Ser Asp Ile Thr Ser Met Ala Glu Gly Glu Leu Ala Ala Lys Leu			
465	470	475	480
Thr Ser Phe Met Phe Gly His Val Val Asn Phe Val Ile Ile Leu Ile			
485	490	495	
Val Ile Leu Phe Leu Tyr Cys Met Ile Arg Asn Arg Asn Arg Gln Tyr			
500	505	510	